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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/747,155

DATE: 08/16/2001

TIME: 13:54:51

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Output Set: N:\CRF3\08162001\I747155.raw

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3 <110> APPLICANT: Rouquier, Sylvie  
4 Giorgi, Dominique  
6 <120> TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same  
8 <130> FILE REFERENCE: 19904-008 (C009B6834US)  
10 <140> CURRENT APPLICATION NUMBER: 09/747,155  
11 <141> CURRENT FILING DATE: 2000-12-21  
13 <150> PRIOR APPLICATION NUMBER: 60/171,746  
14 <151> PRIOR FILING DATE: 1999-12-22  
16 <160> NUMBER OF SEQ ID NOS: 431  
18 <170> SOFTWARE: PatentIn version 3.0  
20 <210> SEQ ID NO: 1  
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22 <212> TYPE: DNA  
23 <213> ORGANISM: Papio hamadryas  
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27 <222> LOCATION: (1)..(649)  
28 <223> OTHER INFORMATION: Taxon = 9557; gene = PPA13; Accession DDBJ/EMBL/GenBank =  
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30 <220> FEATURE:  
31 <221> NAME/KEY: CDS  
32 <222> LOCATION: (2)..(649)  
33 <223> OTHER INFORMATION: Product = olfactory receptor  
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38 1 5 10 15  
40 aac atc cag acc aag aac aaa acg att tct tac atg gac tgc ctc acc 97  
41 Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr  
42 20 25 30  
44 cag gtc tat ttc tcc atg ttt ttt cct att ctg ggc aca cta ctc ctg 145  
45 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Gly Thr Leu Leu Leu  
46 35 40 45  
48 acc gtg atg gcc tat gac cgg ttt gtg gcc gtc tgc cac ccc ctg cac 193  
49 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His  
50 50 55 60  
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53 Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val  
54 65 70 75 80  
56 acg tgg ctc att ggt gtc atg acg tcc ctc ctc cat att tct ctg atg 289  
57 Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met  
58 85 90 95  
60 aca cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc 337  
61 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys  
62 100 105 110  
64 gaa ctg aca cat atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac 385  
65 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn  
66 115 120 125

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68 agc acg ttg ata tat gtt atg acg ggt gtg ctg ggc gtt ttt ccc ctc      433
69 Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
70      130      135      140
72 ctt ggg atc att ttc tct tat tca cga atc gct tca tcc ata agg aag      481
73 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
74 145      150      155      160
76 atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct      529
77 Met Ser Ser Ser Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
78      165      170      175
80 cac ctc tcc gtc gtt tct tta ttt tat ggg aca ggc att ggg gtc cac      577
81 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
82      180      185      190
84 ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg      625
85 Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
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109      20      25      30
112 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Gly Thr Leu Leu Leu
113      35      40      45
116 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
117      50      55      60
120 Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
121 65      70      75      80
124 Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
125      85      90      95
128 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
129      100      105      110
132 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
133      115      120      125
136 Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
137      130      135      140
140 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
141 145      150      155      160
144 Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
145      165      170      175

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148 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
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152 Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
153          195          200          205
156 Val Met Tyr Thr Val Val Thr Pro
157          210          215
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163 <213> ORGANISM: Papio hamadryas
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175 cgcatgtatg gaaagtctgc tcctggctgt gatggcctat gaccggtttg tggccatctg      180
177 tcacccccta cactgcccag tcatcatgaa cccacgcctt tgtggctttt tagtttttgt      240
179 gtcttttctt cttagcctgt tggattccca gctacacaat ttgattgtgt tacaacttac      300
181 ctgcttcaat gatgtggaat tctctaaatt tttctgtgac ccttctcaac ttctcaatcc      360
183 tagcctgctc tgacacataa catagtctga tattttattg gtaccatatt tggttttctt      420
185 cctctctcag ggatcctttt cttttactat aaaattgttt cctccattcc gagagttcgc      480
187 tcttcaggta ggaagtataa agccttctcc acctgcagct ctcacctttc agttgtttgc      540
189 ttattttatg gaacagccct tggagggtac ctcagttcag ctgtctctct cccccccagg      600
191 aagggtgcag cggcctcagt gatgtacatg gtggtcaccc cc                        642
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206 <222> LOCATION: (2)..(649)
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212   1          5          10          15
214 aac atc cag acc aag aac aaa acg att tct tac atg gac tgc ctc acc      97
215 Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
216          20          25          30
218 cag gtc tat ttc tcc atg ttt ttt cct att ctg gac aca cta ctc ctg      145
219 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
220          35          40          45
222 acc gtg atg gcc tat gac cgg ttt gtg gcc gtc tgc cac ccc ctg cac      193

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227 Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
228 65                      70                      75                      80
230 acg tgg ctc att ggt gtc atg aca tcc ctc ctc cat att tct ctg atg      289
231 Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
232      85                      90                      95
234 aca cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc      337
235 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
236      100                      105                      110
238 gaa ctg aca cat atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac      385
239 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
240      115                      120                      125
242 agc acg ttg ata tat gtt atg acg ggt gtg ctg ggc gtt ttt ccc ctc      433
243 Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
244      130                      135                      140
246 ctt ggg atc att ttc tct tat tca cga atc gct tca tcc ata agg aag      481
247 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
248 145                      150                      155                      160
250 atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct      529
251 Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
252      165                      170                      175
254 cac ctc tcc gtc gtt tct tta ttt tat ggg aca ggc att ggg gtc cac      577
255 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
256      180                      185                      190
258 ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg      625
259 Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
260      195                      200                      205
262 gtg atg tac acg gtg gtt acc ccc      649
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264      210                      215
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283      20                      25                      30
286 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
287      35                      40                      45
290 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
291      50                      55                      60

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294 Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
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298 Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
299 85 90 95
302 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Cys
303 100 105 110
306 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
307 115 120 125
310 Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
311 130 135 140
314 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
315 145 150 155 160
318 Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
319 165 170 175
322 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
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334 &lt;210&gt; SEQ ID NO: 6

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340 &lt;221&gt; NAME/KEY: misc\_feature

341 &lt;222&gt; LOCATION: (1)..(649)

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AF27817

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345 &lt;221&gt; NAME/KEY: CDS

346 &lt;222&gt; LOCATION: (2)..(649)

347 &lt;223&gt; OTHER INFORMATION: Product = olfactory receptor

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352 1 5 10 15
354 aac atc cag acc aag aac aaa acg att tct tac atg gac tgc ctc acc      97
355 Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
356 20 25 30
358 cag gtc tat ttc tcc atg ttt ttt cct att ctg gac aca cta ctc ctg      145
359 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
360 35 40 45
362 acc gtg atg gcc tat gac cgg ttt gtg gcc atc tat cac tcc ctg cac      193
363 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Tyr His Ser Leu His
364 50 55 60
366 tac acg gtc atc atg agc ccc cgg ctc tgt gga ctg ctg gtt ctg gga      241
367 Tyr Thr Val Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Leu Gly
368 65 70 75 80
370 tcc tgg tgc atc agt gtc atg ggt tcc ctg ctt gag acc ttg act gtt      289

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**VERIFICATION SUMMARY**

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